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SEQUENCE LISTING

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JAN 07 2004
TECH-CENTER 1600/2900

<110> Wright, David A.
Voytas, Daniel F.

<120> PLANT RETROELEMENTS AND METHODS RELATED THERETO

<130> 08411-030002

<140> 09/965,553

<141> 2001-09-27

<150> 09/322,478

<151> 1999-05-28

<150> 60/087,125

<151> 1998-05-29

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<213> Artificial Sequence

<220>

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cctccagacc atgatgccat cctttccgct ctgtgtactc cagggggacg atttgttctg 480
aatgttgata gtgccccctg gaagctgctg cggaaggatc tgatgacgct cgcgcagaca 540
tgagtggtgc tctcttattt taaccttgca ctgacttttc acacttctga tattaatgtt 600
gacagggccc gactcaatta tggcttgggt atgaagatgg acctggacgt gggcagcctc 660
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Gln Asp Ser Ile Gln Leu Arg Asn Ile Leu Pro Glu Arg Asn Val Glu
35 40 45
Leu Gly Pro Gly Met Phe Asp Glu Phe Leu Gln Glu Leu Gln Arg Leu
50 55 60
Arg Trp Asp Gln Val Leu Thr Arg Leu Pro Glu Lys Trp Ile Asp Val
65 70 75 80
Ala Leu Val Lys Glu Phe Tyr Ser Asn Leu Tyr Asp Pro Glu Asp His
85 90 95
Ser Pro Lys Phe Trp Ser Val Arg Gly Gln Val Val Arg Phe Asp Ala

	100		105		110
Glu Thr Ile Asn Asp Phe Leu Asp Thr Pro Val Ile Leu Ala Glu Gly					
	115		120		125
Glu Asp Tyr Pro Ala Tyr Ser Gln Tyr Leu Ser Thr Pro Pro Asp His					
	130		135		140
Asp Ala Ile Leu Ser Ala Leu Cys Thr Pro Gly Gly Arg Phe Val Leu					
145		150		155	160
Asn Val Asp Ser Ala Pro Trp Lys Leu Leu Arg Lys Asp Leu Met Thr					
	165		170		175
Leu Ala Gln Thr Trp Ser Val Leu Ser Tyr Phe Asn Leu Ala Leu Thr					
	180		185		190
Phe His Thr Ser Asp Ile Asn Val Asp Arg Ala Arg Leu Asn Tyr Gly					
	195		200		205
Leu Val Met Lys Met Asp Leu Asp Val Gly Ser Leu Ile Ser Leu Gln					
	210		215		220
Ile Ser Gln Ile Ala Gln Ser Ile Thr Ser Arg Leu Gly Phe Pro Ala					
225		230		235	240
Leu Ile Thr Thr Leu Cys Glu Ile Gln Gly Val Val Ser Asp Thr Leu					
	245		250		255
Ile Phe Glu Ser Leu Ser Pro Val Ile Asn Leu Ala Tyr Ile Lys Lys					
	260		265		270
Asn Cys Trp Asn Pro Ala Asp Pro Ser Ile Thr Phe Gln Gly Thr Arg					
	275		280		285
Arg Thr Arg Thr Arg Ala Ser Ala Ser Ala Ser Glu Ala Pro Leu Pro					
	290		295		300
Ser Gln His Pro Ser Gln Pro Phe Ser Gln Arg Pro Arg Pro Pro Leu					
305		310		315	320
Leu Ser Thr Ser Ala Pro Pro Tyr Met His Gly Gln Met Leu Arg Ser					
	325		330		335
Leu Tyr Gln Gly Gln Gln Ile Ile Ile Gln Asn Leu Tyr Arg Leu Ser					
	340		345		350
Leu His Leu Gln Met Asp Leu Pro Leu Met Thr Pro Glu Ala Tyr Arg					
	355		360		365
Gln Gln Val Ala Lys Leu Gly Asp Gln Pro Ser Thr Asp Arg Gly Glu					
	370		375		380
Glu Pro Ser Gly Ala Ala Ala Thr Glu Asp Pro Ala Val Asp Glu Asp					
385		390		395	400
Leu Ile Ala Asp Leu Ala Gly Ala Asp Trp Ser Pro Trp Ala Asp Leu					
	405		410		415
Gly Arg Gly Ser Glx					
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<211> 1596

<212> DNA

<213> Artificial Sequence

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<223> plant retroelement sequence

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acctcacctc ctccttctcc aaattatgct cagatggacg gggaaccggc acaaagagtc	180
acactagagg acttctctaa taccaccact cctcagttct ttacaagtat cacaaggccg	240
gaagtccaag cagatctcct tactcaaggg aacctcttcc atggtcttcc aaatgaagat	300
ccatatgcgc atctagcctc atacatagag atatgcagca ccgttaaaat cgccggaggtt	360

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ccaaaagatg cgatactcct taacctcttt tccttttccc tagcaggaga ggcaaaaaga 420
tggttgact cctttaaagg caatagctta agaacatggg aagaagtagt ggaaaaattc 480
ttaaagaagt atttcccaga gtcaaagacc gtcgaacgaa agatggagat ttcttatttc 540
catcaatttc tggatgaatc ccttagcgaa gcactagacc atttccacgg attgctaaga 600
aaaacaccaa cacacagata cagcgagcca gtacaactaa acatattcat cgatgacttg 660
caactcttaa tcgaaacagc tactagaggg aagatcaagc tgaagactcc cgaagaagcg 720
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gttcccacaa aaagaagcct cttggagctt agcacgcagg acgcaacttt ggtacaaaac 840
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ttacaagcga taagtcttc ccactcttct gttttgcagg tagaagaatg ccccatatgc 960
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ttcaatcaag gggcaacaag atttaatcac gagccaccgg ggtttaatca aggaagaaac 1140
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<210> 8
 <211> 532
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 <213> Artificial Sequence

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 <223> plant retroelement sequence

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<400> 8
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          20             25             30
Gln Asp Ile Glu Gly Ser Ser Tyr Thr Ser Pro Pro Pro Ser Pro Asn
          35             40             45
Tyr Ala Gln Met Asp Gly Glu Pro Ala Gln Arg Val Thr Leu Glu Asp
          50             55             60
Phe Ser Asn Thr Thr Thr Pro Gln Phe Phe Thr Ser Ile Thr Arg Pro
65             70             75             80
Glu Val Gln Ala Asp Leu Leu Thr Gln Gly Asn Leu Phe His Gly Leu
          85             90             95
Pro Asn Glu Asp Pro Tyr Ala His Leu Ala Ser Tyr Ile Glu Ile Cys
          100            105            110
Ser Thr Val Lys Ile Ala Gly Val Pro Lys Asp Ala Ile Leu Leu Asn
          115            120            125
Leu Phe Ser Phe Ser Leu Ala Gly Glu Ala Lys Arg Trp Leu His Ser
          130            135            140
Phe Lys Gly Asn Ser Leu Arg Thr Trp Glu Glu Val Val Glu Lys Phe
145            150            155            160
Leu Lys Lys Tyr Phe Pro Glu Ser Lys Thr Val Glu Arg Lys Met Glu
          165            170            175
Ile Ser Tyr Phe His Gln Phe Leu Asp Glu Ser Leu Ser Glu Ala Leu
          180            185            190
Asp His Phe His Gly Leu Leu Arg Lys Thr Pro Thr His Arg Tyr Ser
          195            200            205

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Glu Pro Val Gln Leu Asn Ile Phe Ile Asp Asp Leu Gln Leu Leu Ile
 210 215 220
 Glu Thr Ala Thr Arg Gly Lys Ile Lys Leu Lys Thr Pro Glu Glu Ala
 225 230 235 240
 Met Glu Leu Val Glu Asn Met Ala Ala Ser Asp Gln Ala Ile Leu His
 245 250 255
 Asp His Thr Tyr Val Pro Thr Lys Arg Ser Leu Leu Glu Leu Ser Thr
 260 265 270
 Gln Asp Ala Thr Leu Val Gln Asn Lys Leu Leu Thr Arg Gln Ile Glu
 275 280 285
 Ala Leu Ile Glu Thr Leu Ser Lys Leu Pro Gln Gln Leu Gln Ala Ile
 290 295 300
 Ser Ser Ser His Ser Ser Val Leu Gln Val Glu Glu Cys Pro Thr Cys
 305 310 315 320
 Arg Gly Thr His Glu Pro Gly Gln Cys Ala Ser Gln Gln Asp Pro Ser
 325 330 335
 Arg Glu Val Asn Tyr Ile Gly Ile Leu Asn Arg Tyr Gly Phe Gln Gly
 340 345 350
 Tyr Asn Gln Gly Asn Pro Ser Gly Phe Asn Gln Gly Ala Thr Arg Phe
 355 360 365
 Asn His Glu Pro Pro Gly Phe Asn Gln Gly Arg Asn Phe Met Gln Gly
 370 375 380
 Ser Ser Trp Thr Asn Lys Gly Asn Gln Tyr Lys Glu Gln Arg Asn Gln
 385 390 395 400
 Pro Pro Tyr Gln Pro Pro Tyr Gln His Pro Ser Gln Gly Pro Asn Gln
 405 410 415
 Gln Glu Lys Pro Thr Lys Ile Glu Glu Leu Leu Leu Gln Phe Ile Lys
 420 425 430
 Glu Thr Arg Ser His Gln Lys Ser Thr Asp Ala Ala Ile Arg Asn Leu
 435 440 445
 Glu Val Gln Met Gly Gln Leu Ala His Asp Lys Ala Glu Arg Pro Thr
 450 455 460
 Arg Thr Phe Gly Ala Asn Met Glu Arg Arg Thr Pro Arg Lys Asp Lys
 465 470 475 480
 Ala Val Leu Thr Arg Gly Gln Arg Arg Ala Gln Glu Glu Gly Lys Val
 485 490 495
 Glu Gly Glu Asp Trp Pro Glu Glu Gly Arg Thr Glu Lys Thr Glu Glu
 500 505 510
 Glu Glu Lys Val Ala Glu Glu Pro Lys Arg Thr Lys Ser Gln Arg Ala
 515 520 525
 Arg Glu Ala Lys
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<211> 603

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<213> Artificial Sequence

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tcatacggga atgtctacat cttggtagct gtggattacg tctccaaatg ggtggaagcc	180
atagccacgc caaaggacga tgccagggtg gtgatcaaat ttctgaagaa gaacattttt	240
tcccgttttg gagtcccacg agccttgatt agtgataggg gaacgcactt ctgcaacaat	300

cagttgaaga aagtcctgga gcactataat gtccgacata aggtggccac accttatcac	360
cctcagacaa atggccaagc agaaatttct aacagggagc tcaagcgaat cctggaaaag	420
acagttgcat caacaagaaa ggattggtcc ttgaagctcg atgatgctct ctgggcctat	480
aggacagcgt tcaagactcc catcggctta tcaccatttc agctagtgtg tgggaaggca	540
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gac	603

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Pro	Leu	Gln	Asn	Ile	Met	Glu	Val	Glu	Ile	Phe	Asp	Cys	Trp	Gly	Ile		
			20					25					30				
Asp	Phe	Met	Gly	Pro	Phe	Pro	Ser	Ser	Tyr	Gly	Asn	Val	Tyr	Ile	Leu		
		35					40					45					
Val	Ala	Val	Asp	Tyr	Val	Ser	Lys	Trp	Val	Glu	Ala	Ile	Ala	Thr	Pro		
		50				55					60						
Lys	Asp	Asp	Ala	Arg	Val	Val	Ile	Lys	Phe	Leu	Lys	Lys	Asn	Ile	Phe		
65				70					75				80				
Ser	Arg	Phe	Gly	Val	Pro	Arg	Ala	Leu	Ile	Ser	Asp	Arg	Gly	Thr	His		
			85					90					95				
Phe	Cys	Asn	Asn	Gln	Leu	Lys	Lys	Val	Leu	Glu	His	Tyr	Asn	Val	Arg		
		100						105					110				
His	Lys	Val	Ala	Thr	Pro	Tyr	His	Pro	Gln	Thr	Asn	Gly	Gln	Ala	Glu		
		115				120						125					
Ile	Ser	Asn	Arg	Glu	Leu	Lys	Arg	Ile	Leu	Glu	Lys	Thr	Val	Ala	Ser		
		130				135					140						
Thr	Arg	Lys	Asp	Trp	Ser	Leu	Lys	Leu	Asp	Asp	Ala	Leu	Trp	Ala	Tyr		
145				150					155				160				
Arg	Thr	Ala	Phe	Lys	Thr	Pro	Ile	Gly	Leu	Ser	Pro	Phe	Gln	Leu	Val		
			165					170					175				
Tyr	Gly	Lys	Ala	Cys	His	Leu	Pro	Val	Glu	Leu	Glu	Tyr	Lys	Ala	Tyr		
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Trp	Ala	Leu	Lys	Leu	Leu	Asn	Phe	Asp									
		195				200											

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cgaactgtca	ctggttggcg	aatgtgtatc	gactatcgca	agctgaatga	agccacacgg				180
aaggaccatt	ttcccttacc	tttcatggat	cagatgctgg	agagacttgc	agggcaggca				240
tactactgtt	tcttggatgg	atactcggga	tacaaccaga	tcgcggtaga	ccccagagat				300

caggagaaga	cggcctttac	atgccccctt	ggcgtctttg	cttacagaag	gatgccattc	360
gggttatgta	atgcaccagc	cacatttcag	aggtgcatgc	tggccatttt	ttcagacatg	420
gtggagaaaa	gcatcgaggt	atztatggac	gacttctcgg	tttttggacc	ctcatttgac	480
agctgtttga	ggaacctaga	gagggactct	cagaggtgcg	aagagactaa	cttggtactg	540
aattgggaaa	agtgtcattt	catggttcga	gagggcatag	tcctaggcca	caagatctca	600

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<211> 200

<212> PRT

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<400> 12

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Pro	Val	Gln	Val	Val	Pro	Lys	Lys	Gly	Gly	Met	Thr	Val	Val	Arg	Asp
			20					25					30		
Glu	Arg	Asn	Asp	Leu	Ile	Pro	Thr	Arg	Thr	Val	Thr	Gly	Trp	Arg	Met
		35					40					45			
Cys	Ile	Asp	Tyr	Arg	Lys	Leu	Asn	Glu	Ala	Thr	Arg	Lys	Asp	His	Phe
	50					55					60				
Pro	Leu	Pro	Phe	Met	Asp	Gln	Met	Leu	Glu	Arg	Leu	Ala	Gly	Gln	Ala
65					70					75				80	
Tyr	Tyr	Cys	Phe	Leu	Asp	Gly	Tyr	Ser	Gly	Tyr	Asn	Gln	Ile	Ala	Val
			85					90					95		
Asp	Pro	Arg	Asp	Gln	Glu	Lys	Thr	Ala	Phe	Thr	Cys	Pro	Phe	Gly	Val
			100					105					110		
Phe	Ala	Tyr	Arg	Arg	Met	Pro	Phe	Gly	Leu	Cys	Asn	Ala	Pro	Ala	Thr
		115					120					125			
Phe	Gln	Arg	Cys	Met	Leu	Ala	Ile	Phe	Ser	Asp	Met	Val	Glu	Lys	Ser
	130					135					140				
Ile	Glu	Val	Phe	Met	Asp	Phe	Ser	Val	Phe	Gly	Pro	Ser	Phe	Asp	
145				150					155					160	
Ser	Cys	Leu	Arg	Asn	Leu	Glu	Arg	Val	Leu	Gln	Arg	Cys	Glu	Glu	Thr
			165					170					175		
Asn	Leu	Val	Leu	Asn	Trp	Glu	Lys	Cys	His	Phe	Met	Val	Arg	Glu	Gly
		180						185					190		
Ile	Val	Leu	Gly	His	Lys	Ile	Ser								
		195					200								

<210> 13

<211> 858

<212> DNA

<213> Artificial Sequence

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<223> plant retroelement sequence

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ccattcgggg	aagccttaca	gcagatgccc	ctctactcca	aatttatgaa	agacatcctc	180
accaagaagg	ggaagtatat	tgacaacgag	aatattgtgg	taggaggcaa	ttgcagtgcg	240
ataatacaaa	ggattctacc	caagaagttt	aaagaccccc	gaagtgttac	catcccgtgc	300
accattggga	aggaagccgt	aaacaaggcc	ctcattgatc	taggagcaag	tatcaatctg	360


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cttcaactgg cagaccgctc aatcacaagg ccatatgggg tggtagaaga tgtcctgggc 480
aaggtacgcc acttcacttt tccggtggac tttgttatca tggatatcga agaagacact 540
gagattcccc ttatcttagg cagacccttc atgctgactg ccaactgtgt ggtggatatg 600
gggaaaggga acttagagtt gactattgat aatcagaaga tcaccttga cttatcaag 660
gcaatgaagt acccacagga gggttggaag tgcttcagaa tagaggagat tgatgaggaa 720
gatgtcagtt ttctcgagac accaaagact tcgctagaaa aagcaatggg aaatcattta 780
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<210> 14

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<213> Artificial Sequence

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20          25          30
Phe Lys Gly Leu Glu Ile Thr Met Pro Phe Gly Glu Ala Leu Gln Gln
35          40          45
Met Pro Leu Tyr Ser Lys Phe Met Lys Asp Ile Leu Thr Lys Lys Gly
50          55          60
Lys Tyr Ile Asp Asn Glu Asn Ile Val Val Gly Asn Cys Ser Ala
65          70          75          80
Ile Ile Gln Arg Ile Leu Pro Lys Lys Phe Lys Asp Pro Gly Ser Val
85          90          95
Thr Ile Pro Cys Thr Ile Gly Lys Glu Ala Val Asn Lys Ala Leu Ile
100         105         110
Asp Leu Gly Ala Ser Ile Asn Leu Met Pro Leu Ser Met Cys Lys Arg
115         120         125
Ile Gly Asn Leu Lys Ile Asp Pro Thr Lys Met Thr Leu Gln Leu Ala
130         135         140
Asp Arg Ser Ile Thr Arg Pro Tyr Gly Val Val Glu Asp Val Leu Val
145         150         155         160
Lys Val Arg His Phe Thr Phe Pro Val Asp Phe Val Ile Met Asp Ile
165         170         175
Glu Glu Asp Thr Glu Ile Pro Leu Ile Leu Gly Arg Pro Phe Met Leu
180         185         190
Thr Ala Asn Cys Val Val Asp Met Gly Lys Gly Asn Leu Glu Leu Thr
195         200         205
Ile Asp Asn Gln Lys Ile Thr Phe Asp Leu Ile Lys Ala Met Lys Tyr
210         215         220
Pro Gln Glu Gly Trp Lys Cys Phe Arg Ile Glu Glu Ile Asp Glu Glu
225         230         235         240
Asp Val Ser Phe Leu Glu Thr Pro Lys Thr Ser Leu Glu Lys Ala Met
245         250         255
Val Asn His Leu Asp Cys Leu Thr Ser Glu Glu Glu Glu Asp Leu Lys
260         265         270
Ala Cys Leu Glu Asn Leu Asp Gln Glu Asp Ser Ile Pro Glu
275         280         285

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 tatgcaacca cagaaaagga gatgctagcc attgtctttg ccttggagaa gttcaggtca 180
 tacttgatag gg 192

<210> 16
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 <212> PRT
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 <223> plant retroelement sequence

<400> 16
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 20 25 30
 Val Leu Asn Glu Ala Gln Leu Asn Tyr Ala Thr Thr Glu Lys Glu Met
 35 40 45
 Leu Ala Ile Val Phe Ala Leu Glu Lys Phe Arg Ser Tyr Leu Ile Gly
 50 55 60

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 <211> 12286
 <212> DNA
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Gln	Asp	Ile	Glu	Gly	Ser	Ser	Tyr	Thr	Ser	Pro	Pro	Pro	Ser	Pro	Asn
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Phe	Ser	Asn	Thr	Thr	Thr	Pro	Gln	Phe	Phe	Thr	Ser	Ile	Thr	Arg	Pro
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Glu	Val	Gln	Ala	Asp	Leu	Leu	Thr	Gln	Gly	Asn	Leu	Phe	His	Gly	Leu
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Ser	Thr	Val	Lys	Ile	Ala	Gly	Val	Pro	Lys	Asp	Ala	Ile	Leu	Leu	Asn
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Leu	Phe	Ser	Phe	Ser	Leu	Ala	Gly	Glu	Ala	Lys	Arg	Trp	Leu	His	Ser
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Asp	His	Phe	His	Gly	Leu	Leu	Arg	Lys	Thr	Pro	Thr	His	Arg	Tyr	Ser
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Glu	Thr	Ala	Thr	Arg	Gly	Lys	Ile	Lys	Leu	Lys	Thr	Pro	Glu	Glu	Ala
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Met	Glu	Leu	Val	Glu	Asn	Met	Ala	Ala	Ser	Asp	Gln	Ala	Ile	Leu	His
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Asp	His	Thr	Tyr	Val	Pro	Thr	Lys	Arg	Ser	Leu	Leu	Glu	Leu	Ser	Thr
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Arg	Gly	Thr	His	Glu	Pro	Gly	Gln	Cys	Ala	Ser	Gln	Gln	Asp	Pro	Ser
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Tyr	Pro	Met	Ala	Pro	Thr	Lys	Lys	Asn	Lys	Glu	Arg	Tyr	Phe	Ala	Arg
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Phe	Leu	Glu	Ile	Phe	Lys	Gly	Leu	Glu	Ile	Thr	Met	Pro	Phe	Gly	Glu
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Thr	Lys	Lys	Gly	Lys	Tyr	Ile	Asp	Asn	Glu	Asn	Ile	Val	Val	Gly	Gly
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Lys	Ala	Leu	Ile	Asp	Leu	Gly	Ala	Ser	Ile	Asn	Leu	Met	Pro	Leu	Ser
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 Arg Arg Phe Ile Lys Asp Phe Ser Lys Ile Ala Arg Pro Leu Ser Asn
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 Val Arg His Lys Val Ala Thr Pro Tyr His Pro Gln Thr Asn Gly Gln

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Ala Ser Thr Arg Lys Asp Trp Ser Leu Lys Leu Asp Asp Ala Leu Trp						
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Ala Tyr Arg Thr Ala Phe Lys Thr Pro Ile Gly Leu Ser Pro Phe Gln						
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Asn Gly Gln Arg Leu Lys Pro Tyr Asn Gly Gly Gln Leu Glu Arg Leu						
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<210> 19

<211> 9829

<212> DNA

<213> Glycine max

<400> 19

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<211> 1857

<212> DNA

<213> Arabidopsis thaliana

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<211> 564

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<211> 180

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<213> Arabidopsis thaliana

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<211> 192

<212> DNA

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<212> DNA

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 <213> Pisum sativum

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<400> 36	
cctaaaatac	tacaacgaca
caatttggcg	ccgttgccaa
	60
	120

tagatcaagt tctttttcaa ttttcttttt	150
<210> 37	
<211> 11	
<212> DNA	
<213> Glycine max	
<400> 37	
tggcgccgtt g	11
<210> 38	
<211> 15	
<212> DNA	
<213> Glycine max	
<400> 38	
tggcgccgtt gccgg	15
<210> 39	
<211> 27	
<212> DNA	
<213> Glycine max	
<400> 39	
tttttggcgc cgttgtcggg gattttg	27
<210> 40	
<211> 9	
<212> DNA	
<213> Glycine max	
<400> 40	
tttggggga	9
<210> 41	
<211> 16	
<212> DNA	
<213> Glycine max	
<400> 41	
tttaatttgg gggatt	16
<210> 42	
<211> 20	
<212> DNA	
<213> Artificial Sequence	
<220>	
<223> primer	
<400> 42	
gggatccgca attagaatct	20
<210> 43	
<211> 20	
<212> DNA	
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<220>
 <223> primer

 <400> 43
 cgaattcggg ccacttcgga 20

 <210> 44
 <211> 24
 <212> DNA
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 <220>
 <223> primer

 <400> 44
 ccacaagatt ctaattgcgg attc 24

 <210> 45
 <211> 24
 <212> DNA
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 <220>
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 <400> 45
 ccgaaatgga ccgaaccgga catc 24

 <210> 46
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>
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 <400> 46
 tttccaggct cttgacgaga tttg 24

 <210> 47
 <211> 22
 <212> DNA
 <213> Artificial Sequence

 <220>
 <223> primer

 <400> 47
 cgactcgagc tccatagcga tg 22

 <210> 48
 <211> 24
 <212> DNA
 <213> Artificial Sequence

 <220>

<223> primer

<400> 48

cggattgggc cgaaatggac cgaa

24

<210> 49

<211> 18

<212> DNA

<213> Arabidopsis thaliana

<400> 49

gaggacttgg ggggcaaa

18

<210> 50

<211> 13

<212> PRT

<213> Artificial Sequence

<220>

<223> exemplary motif

<221> VARIANT

<222> 2-3, 5-7, 9-12

<223> Xaa = Any Amino Acid

<400> 50

Cys Xaa Xaa Cys Xaa Xaa Xaa His Xaa Xaa Xaa Xaa Cys

1

5

10

<210> 51

<211> 6

<212> PRT

<213> Artificial Sequence

<220>

<223> exemplary motif

<400> 51

Leu Ile Asp Leu Gly Ala

1

5

<210> 52

<211> 4

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<400> 52

Lys Thr Ala Phe

1

<210> 53

<211> 8

<212> PRT

<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> 2
<223> Xaa = Pro or Ser

<400> 53
Met Xaa Phe Gly Leu Cys Asn Ala
1 5

<210> 54
<211> 10
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> 1
<223> Xaa = Val, Ile, or Met

<221> VARIANT
<222> 9
<223> Xaa = Ser or Trp

<221> VARIANT
<222> 10
<223> Xaa = Val or Ile

<400> 54
Xaa Glu Val Phe Met Asp Asp Phe Xaa Xaa
1 5 10

<210> 55
<211> 19
<212> PRT
<213> Artificial Sequence

<220>
<223> consensus sequence

<221> VARIANT
<222> 12
<223> Xaa = Ile or Val

<400> 55
Phe Glu Leu Met Cys Asp Ala Ser Asp Tyr Ala Xaa Gly Ala Val Leu
1 5 10 15
Gly Gln Arg

<210> 56
<211> 27
<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 4

<223> Xaa = Thr or Ile

<221> VARIANT

<222> 8

<223> Xaa = Leu or Met

<221> VARIANT

<222> 13

<223> Xaa = Phe or Tyr

<221> VARIANT

<222> 15

<223> Xaa = Leu or Phe

<221> VARIANT

<222> 19

<223> Xaa = Arg or Lys

<221> VARIANT

<222> 23

<223> Xaa = Ile or Val

<221> VARIANT

<222> 26

<223> Xaa = Arg or Lys

<400> 56

Tyr	Ala	Thr	Xaa	Glu	Lys	Glu	Xaa	Leu	Ala	Ile	Val	Xaa	Ala	Xaa	Glu
1				5				10						15	
Lys	Phe	Xaa	Ser	Tyr	Leu	Xaa	Gly	Ser	Xaa	Val					
			20				25								

<210> 57

<211> 46

<212> PRT

<213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 4, 6-7, 11-40, 43

<223> Xaa = Any Amino Acid

<400> 57

His	Cys	His	Xaa	Ser	Xaa	Xaa	Gly	Gly	His	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
1				5				10					15		
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa
			20				25					30			
Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Xaa	Cys	Asp	Xaa	Cys	Gln	Arg		

35

40

45

<210> 58
 <211> 8
 <212> PRT
 <213> Artificial Sequence

 <220>
 <223> consensus sequence

 <221> VARIANT
 <222> 6
 <223> Xaa = Ile, Val, or Met

 <400> 58
 Trp Gly Ile Asp Phe Xaa Gly Pro
 1 5

<210> 59
 <211> 11
 <212> PRT
 <213> Artificial Sequence

<220>
 <223> consensus sequence

 <221> VARIANT
 <222> 7
 <223> Xaa = Any Amino Acid

<221> VARIANT
 <222> 10
 <223> Xaa = Ala or Val

<400> 59
 Pro Tyr His Pro Gln Thr Xaa Gly Gln Xaa Glu
 1 5 10

<210> 60
 <211> 13
 <212> DNA
 <213> Artificial Sequence

<220>
 <223> consensus sequence

<221> misc_feature
 <222> 11, 12
 <223> n = A,T,C or G

<400> 60
 atttgggggra nnt

13

<210> 61
 <211> 9
 <212> PRT
 <213> Artificial Sequence

<220>

<223> consensus sequence

<221> VARIANT

<222> 5, 8

<223> Xaa = Arg or Lys

<400> 61

Gln Met Ala Ser Xaa Lys Arg Xaa Ala
1 5

<210> 62

<211> 6

<212> PRT

<213> Pisum sativum

<400> 62

Ala Ser Lys Lys Arg Lys
1 5